

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 17, 2003. 09:13:37 ; Search time 3691 Seconds
(without alignments)
10496.184 Million call updates/sec.

Title: US-10-043-539A-1

Perfect score: 947

Sequence: 1 gtttccaaatccgtggagg.....gtttccaaatccgtggatcgat 947

Scoring table: IDENTITY_NUC Gapop 10-0 . Gapext 1.0

Searched: 288711 seqs, 204581386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_ntg:*

3: gb_ln:*

4: gb_cm:*

5: gb_ov:*

6: gb_jat:*

7: gb_bh:*

8: gb_dp:*

9: gb_pr:*

10: gb_zo:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_da:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_nu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_dat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_vl:*

29: em_htg_inv:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrc:*

38: em_sy:*

39: em_htg_hum:*

40: em_htg_mus:*

41: em_htg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|--------------------------------------|
| 1 | 947 | 100.0 | 947 | AF207701 Staphylococcal updates/sec. |
| c | 2 | 86.4 | 1 | AF004829 Staphylococcal |
| c | 3 | 86.4 | 1 | AP003136 Staphylococcal |
| c | 4 | 84.8 | 1 | AP003136 Staphylococcal |
| c | 5 | 39.8 | 6 | AX620460 Sequence |
| c | 6 | 30.7 | 1 | AE016750 Staphylococcal |
| c | 7 | 19.4 | 1 | AX620416 Sequence |
| c | 8 | 96.2 | 6 | AX59046 Sequence |
| c | 9 | 92.8 | 2 | AC125567 Rattus no |
| c | 10 | 91.4 | 9.8 | PMAL1P3 |
| c | 11 | 90.6 | 9.6 | AF466146 Melipona |
| c | 12 | 90.4 | 6 | PMAL1P5 |
| c | 13 | 90 | 9.5 | PMAL1P6 |
| c | 14 | 87.6 | 9.3 | AX59046 Sequence |
| c | 15 | 87.2 | 9.2 | AX59046 Sequence |
| c | 16 | 65.2 | 9.0 | AC117140 Rattus no |
| c | 17 | 85 | 9.0 | CN610848 |
| c | 18 | 84.8 | 9.0 | AX457067 Sequence |
| c | 19 | 84.6 | 8.9 | AE014820 Plasmidu |
| c | 20 | 84.2 | 8.9 | HUAC0405 |
| c | 21 | 83.6 | 8.8 | AC117342 Rattus no |
| c | 22 | 83 | 8.8 | AC092066 Homo sapi |
| c | 23 | 82.8 | 8.7 | AB084761 Drosophil |
| c | 24 | 82.8 | 8.7 | AL928828 Zebrafish |
| c | 25 | 82.4 | 8.7 | AB065521 Wigglewo |
| c | 26 | 82.4 | 8.7 | AX344555 Sequence |
| c | 27 | 82.2 | 8.7 | AC098955 Rattus no |
| c | 28 | 82 | 8.7 | AX251493 |
| c | 29 | 82 | 8.7 | AC093198 Homo sapi |
| c | 30 | 81.6 | 8.6 | AL035756 Plasmidu |
| c | 31 | 81.4 | 8.6 | AC004153 Plasmidu |
| c | 32 | 81.4 | 8.6 | AE014848 Plasmidu |
| c | 33 | 81.4 | 8.6 | AL929511 Plasmidu |
| c | 34 | 81.2 | 8.6 | AL390756 Homo sapi |
| c | 35 | 81 | 8.6 | Continuation (10 o |
| c | 36 | 81.2 | 8.6 | AL049384 Plasmidu |
| c | 37 | 81 | 8.6 | BX005661 Danio rer |
| c | 38 | 81 | 8.6 | BX322349 Danio rer |
| c | 39 | 81 | 8.6 | AC096885 Danio rer |
| c | 40 | 80.8 | 8.5 | AL929512 Plasmidu |
| c | 41 | 80.6 | 8.5 | PMAL1P3 |
| c | 42 | 80.2 | 8.5 | AX598900 Sequence |
| c | 43 | 80.2 | 8.5 | AC023466 Homo sapi |
| c | 44 | 80.2 | 8.5 | AC098822 Homo sapi |
| c | 45 | 80 | 8.4 | AC119418 Medicago |

ALIGNMENTS

RESULT 1
LOCUS AF207701 Staphylococcus aureus putative transposase gene, partial cds; and
DEFINITION Srr (Srr) gene, complete cds.
ACCESSION AF207701
VERSION AF207701.1 GI:11453941
KEYWORDS
SOURCE
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
REFERENCE 1 (bases 1 to 947)
AUTHORS Cheung A.L. and Mana A.C.
TITLE Characterization of Srr, a modulator of sar expression in
Staphylococcus aureus
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
Characterization of Srr, a modulator of sar expression in
Staphylococcus aureus

Pred. No. is the number of results predicted by chance to have a

JOURNAL Unpublished
2 (bases 1 to 947)
AUTHORS Cheung, A.L. and Manna, A.C.
TITLE Direct Submission
SUBMITTED (22-NOV-1999) Microbiology, Dartmouth Medical School,
College St., Vail, 206, Hanover, NH 03755, USA
FEATURES Location/Qualifiers
1. .947
/organism="Staphylococcus aureus"
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208 .55
/gene="sarR"
/note="regulatory gene"
208 .55
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/protein_id="AG3515.1"
/db_xref="GI:11493942"
/translation="MSKINDINDLYNATFOVKKFFDTIKKENLYEYIILHILRS
BSNISSEKEAKCSBFKPYLTKALQKLDSLRSKRSQDERTVIVYVTDOKANI
OKUJSEBEVKN"
BASE COUNT . 374 a 112 c 145 g 316 t
ORIGIN Query Match 100.0% Score 947; DB 1; Length 947;
Best Local Similarity 100.0% Pred. No. 7.e-126;
Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 GTTTCAATCGTGGAGTGTATGAAAAGTTATGGCATTTTGAAATAAAAA 60
1 GTTTCAATCGTGGAGTGTATGAAAAGTTATGGCATTTTGAAATAAAAA 60
Qy 61 ATATCATATAGTTGGACTCATTCGGATTATATCACTTATGGATGACTTA 120
61 ATATCATATAGTTGGACTCATTCGGATTATATCACTTATGGATGACTTA 120
Qy 121 TAACATAGTTGGATAGGTTTCGATTAATCATTAATGTGAACCTCTACAAAG 180
121 TAACATAGTTGGATAGGTTTCGATTAATCATTAATGTGAACCTCTACAAAG 180
Qy 181 ATGGCATAGCAAGGGTGTGGTTATATGGATAAATTAATGGATAAATGGTAC 240
181 ATGGCATAGCAAGGGTGTGGTTATATGGATAAATTAATGGATAAATGGTAC 240
Db 241 AACGGCAATTCGATTAATGGAAACTTTCAGAGATAAAAGAGTCATTCGAAC 300
241 AACGGCAATTCGATTAATGGAAACTTTCAGAGATAAAAGAGTCATTCGAAC 300
Qy 301 TATGGAAATTTATTTTAAATCATATTATGAACTTTCGAGTTAACGAAATCTCT 360
301 TATGGAAATTTATTTTAAATCATATTATGAACTTTCGAGTTAACGAAATCTCT 360
Db 361 AAAGAGATGGCTAACGCTTAGACTTCAACCTTACTTAACTAACGTTACAAAG 420
361 AAAGAGATGGCTAACGCTTAGACTTCAACCTTACTTAACTAACGTTACAAAG 420
Qy 421 CTAAGAGTTAAATGTTATCAAGAAAGAGTTACAGCAAGAAAGCTTAC 480
421 CTAAGAGTTAAATGTTATCAAGAAAGAGTTACAGCAAGAAAGCTTAC 480
Db 481 GTTATGTTACAGATACACAAAGCAAAATTTCAAAACTGTTCAATTAGAGAA 540
Qy

Db 481 GTTATGTTACAGATACACAAAGCAAAATTTCAAAACTGTTCAATTAGAGAA 540
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Db 541 TACATTAATTAATTAATCAAGGTTAAATACATGGATAAACTTGTGATTGAGAA 600
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Db 721 CAAGGTACATCTGCTTTTATTATATTTAGGATGTTACCATCTAA 780
Qy 781 ATATTTTCGCTGATATGATGCTGATGTTGAGCTTCTATAATTTGTCGGA 840
Db 781 ATATTTTCGCTGATATGATGCTGATGTTGAGCTTCTATAATTTGTCGGA 840
Qy 841 TAGGAAATTTCTACTGAAACCATGTTGAGCTTCTATAATTTGTCGGA 900
Db 841 TAGGAAATTTCTACTGAAACCATGTTGAGCTTCTATAATTTGTCGGA 900
Qy 901 TCGGATGTATGCTTAAAGACTTAATGGCTTCAATGTTGATGTTGATCGT 947
Db 901 TCGGATGTATGCTTAAAGACTTAATGGCTTCAATGTTGATGTTGATCGT 947
RESULT 2
AP004829/c
LOCUS AP004829
DEFINITION 304050 bp DNA linear BCR 20-DEC-2002
STaphylococcus aureus subsp. aureus MW2 DNA, complete genome,
strain:MW2, section 8/10.
AP004829 BA000033
AP004829.1 GT:21205117
KEYWORDS
ORGANISM Staphylococcus aureus subsp. aureus MW2
Bacteria: Firmicutes: Bacillales: Staphylococcaceae
REFERENCE Baba, T., Takeuchi, F., Kuroda, M., Yuzawa, H., Aoki, K., Oguchi, A.,
Nagai, Y., Iwama, N., Asano, K., Naimi, T., Kuroda, H., Cui, L.,
Yamamoto, K. and Hiramoto, K.
TITLE Genome and virulence determinants of high virulence
community acquired MRSA
JOURNAL Lancet 359 (9320), 1819-1827 (2002)
MEDLINE 22040717
PUBMED 12044378
REFERENCE 2 (bases 1 to 304050)
AUTHORS Director-General, Biotechnology Center, Aoki, K., Oguchi, A.,
Nagai, Y., Asano, K., Iwama, N., Baba, T., Kuroda, M., Hiramoto, K., and
Kikuchi, H.
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SUBMITTED (06-MAR-2002) Director-General, Biotechnology Center,
Center: 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
(E-mail: bio@mail.bioconite.go.jp, URL: http://www.bio.nite.go.jp/;
Tel: 03-33481-1933, Fax: 03-3481-0424)
FEATURES Location/Qualifiers
1. .304050
/organism="Staphylococcus aureus subsp. aureus MW2"
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/strain:MW2
/db_xref="taxon:196620"
/complement:629..1072
/gene="MW1947"
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/note="ORFID:MW1947"

